

## SEQUENCE LISTING

<110> Degussa AG

5 <120> Process for preparing optically active amino acids using a whole-cell catalyst

<130> 040055 AM

10 <160> 13

<170> PatentIn version 3.1

15 <210> 1  
<211> 47  
<212> DNA  
<213> Artificial

<220>  
20 <223> Primer

<400> 1  
aaaaaactta agaaggagat atacatatga cattagaaat cttcgaa 47

25 <210> 2  
<211> 32  
<212> DNA  
<213> Artificial

30 <220>  
<223> Primer

<400> 2  
35 aaaaaactgc agttagcgac ggctaataat at 32

<210> 3  
<211> 30  
40 <212> DNA  
<213> Artificial

<220>  
<223> Primer

45 <400> 3  
aaaaaacata tgaagattgt cttagttctt 30

50 <210> 4  
<211> 32  
<212> DNA  
<213> Artificial

55 <220>  
<223> Primer

<400> 4  
aaaaaagacg tcttatttct tatcgtgttt ac 32

5 <210> 5  
 <211> 1120  
 <212> DNA  
 <213> Bacillus cereus

10 <220>  
 <221> CDS  
 <222> (20)..(1120)  
 <223>

15 <400> 5  
 ttaagaagga gatatacat atg aca tta gaa atc ttc gaa tac tta gaa aaa 52  
 Met Thr Leu Glu Ile Phe Glu Tyr Leu Glu Lys  
 1 5 10

20 tat gat tat gag caa gta gta ttt tgt caa gat aaa gaa tct ggt tta 100  
 Tyr Asp Tyr Glu Gln Val Val Phe Cys Gln Asp Lys Glu Ser Gly Leu  
 15 20 25

25 aaa gca att att gca att cat gat aca aca ctt gga ccg gct ctt ggt 148  
 Lys Ala Ile Ile Ala Ile His Asp Thr Thr Leu Gly Pro Ala Leu Gly  
 30 35 40

30 gga aca aga atg tgg aca tat gat tct gaa gaa gcg gcg att gaa gat 196  
 Gly Thr Arg Met Trp Thr Tyr Asp Ser Glu Glu Ala Ala Ile Glu Asp  
 45 50 55

35 gca ttg cgt ctt gca aaa ggg atg aca tac aaa aac gca gca gct ggt 244  
 Ala Leu Arg Leu Ala Lys Gly Met Thr Tyr Lys Asn Ala Ala Ala Gly  
 60 65 70 75

40 tta aac tta ggt ggt gcg aaa aca gta att atc ggt gat cct cgt aaa 292  
 Leu Asn Leu Gly Gly Ala Lys Thr Val Ile Ile Gly Asp Pro Arg Lys  
 80 85 90

45 gat aag agc gaa gca atg ttc cgt gca cta gga cgt tat atc caa gga 340  
 Asp Lys Ser Glu Ala Met Phe Arg Ala Leu Gly Arg Tyr Ile Gln Gly  
 95 100 105

50 cta aac gga cgt tac att aca gct gaa gat gtt ggt aca aca gta gat 388  
 Leu Asn Gly Arg Tyr Ile Thr Ala Glu Asp Val Gly Thr Thr Val Asp  
 110 115 120

55 gat atg gat att atc cat gaa gaa act gac ttt gta aca ggt atc tca 436  
 Asp Met Asp Ile Ile His Glu Glu Thr Asp Phe Val Thr Gly Ile Ser  
 125 130 135

60 cca tca ttc ggt tct tct ggt aac cca tct ccg gta act gca tac ggt 484  
 Pro Ser Phe Gly Ser Ser Gly Asn Pro Ser Pro Val Thr Ala Tyr Gly  
 140 145 150 155

65 gtt tac cgt ggt atg aaa gca gct gca aaa gaa gct ttc ggt act gac 532  
 Val Tyr Arg Gly Met Lys Ala Ala Ala Lys Glu Ala Phe Gly Thr Asp  
 160 165 170

70 aat tta gaa gga aaa gta att gct gtt caa ggc gtt ggt aac gta gca 580  
 Asn Leu Glu Gly Lys Val Ile Ala Val Gln Gly Val Gly Asn Val Ala

	175	180	185	
5	tat cac cta tgc aaa cat tta cac gct gaa gga gca aaa tta att gtt Tyr His Leu Cys Lys His Leu His Ala Glu Gly Ala Lys Leu Ile Val 190 195 200			628
10	aca gat att aat aaa gaa gct gta caa cgt gct gta gaa gaa ttc ggt Thr Asp Ile Asn Lys Glu Ala Val Gln Arg Ala Val Glu Glu Phe Gly 205 210 215			676
15	gca tca gca gtt gaa cca aat gaa att tac ggt gtt gaa tgc gat att Ala Ser Ala Val Glu Pro Asn Glu Ile Tyr Gly Val Glu Cys Asp Ile 220 225 230 235			724
20	tac gca cca tgt gca cta ggc gca aca gtt aat gat gaa act att cca Tyr Ala Pro Cys Ala Leu Gly Ala Thr Val Asn Asp Glu Thr Ile Pro 240 245 250			772
25	caa ctt aaa gca aaa gta atc gca ggt tct gcg aat aac caa tta aaa Gln Leu Lys Ala Lys Val Ile Ala Gly Ser Ala Asn Asn Gln Leu Lys 255 260 265			820
30	gaa gat cgt cat ggt gac atc att cat gaa atg ggt att gta tac gca Glu Asp Arg His Gly Asp Ile Ile His Glu Met Gly Ile Val Tyr Ala 270 275 280			868
35	cca gat tat gta att aat gca ggt ggc gta att aac gta gca gac gaa Pro Asp Tyr Val Ile Asn Ala Gly Gly Val Ile Asn Val Ala Asp Glu 285 290 295			916
40	tta tat gga tac aat aga gaa cgt gca cta aaa cgt gtt gag tct att Leu Tyr Gly Tyr Asn Arg Glu Arg Ala Leu Lys Arg Val Glu Ser Ile 300 305 310 315			964
45	tat gac acg att gca aaa gta atc gaa att tca aaa cgc gat ggc ata Tyr Asp Thr Ile Ala Lys Val Ile Glu Ile Ser Lys Arg Asp Gly Ile 320 325 330			1012
50	gca act tat gta gcg gca gat cgt cta gct gaa gag cgc att gca agc Ala Thr Tyr Val Ala Ala Asp Arg Leu Ala Glu Glu Arg Ile Ala Ser 335 340 345			1060
55	ttg aag aat tct cgt agc act tac tta cgc aac ggt cac gat att att Leu Lys Asn Ser Arg Ser Thr Tyr Leu Arg Asn Gly His Asp Ile Ile 350 355 360			1108
60	agc cgt cgc taa Ser Arg Arg 365			1120
65	<210> 6 <211> 366 <212> PRT <213> Bacillus cereus  <400> 6  Met Thr Leu Glu Ile Phe Glu Tyr Leu Glu Lys Tyr Asp Tyr Glu Gln			

	1		5		10		15									
5	Val	Val	Phe	Cys	Gln	Asp	Lys	Glu	Ser	Gly	Leu	Lys	Ala	Ile	Ile	Ala
			20					25						30		
10	Ile	His	Asp	Thr	Thr	Leu	Gly	Pro	Ala	Leu	Gly	Gly	Thr	Arg	Met	Trp
		35						40					45			
15	Thr	Tyr	Asp	Ser	Glu	Glu	Ala	Ala	Ile	Glu	Asp	Ala	Leu	Arg	Leu	Ala
		50					55					60				
20	Lys	Gly	Met	Thr	Tyr	Lys	Asn	Ala	Ala	Ala	Gly	Leu	Asn	Leu	Gly	Gly
	65					70					75				80	
25	Ala	Lys	Thr	Val	Ile	Ile	Gly	Asp	Pro	Arg	Lys	Asp	Lys	Ser	Glu	Ala
				85						90					95	
30	Met	Phe	Arg	Ala	Leu	Gly	Arg	Tyr	Ile	Gln	Gly	Leu	Asn	Gly	Arg	Tyr
				100					105					110		
35	Ile	Thr	Ala	Glu	Asp	Val	Gly	Thr	Thr	Val	Asp	Asp	Met	Asp	Ile	Ile
			115					120					125			
40	His	Glu	Glu	Thr	Asp	Phe	Val	Thr	Gly	Ile	Ser	Pro	Ser	Phe	Gly	Ser
		130					135					140				
45	Ser	Gly	Asn	Pro	Ser	Pro	Val	Thr	Ala	Tyr	Gly	Val	Tyr	Arg	Gly	Met
	145					150					155				160	
50	Lys	Ala	Ala	Ala	Lys	Glu	Ala	Phe	Gly	Thr	Asp	Asn	Leu	Glu	Gly	Lys
				165						170					175	
55	Val	Ile	Ala	Val	Gln	Gly	Val	Gly	Asn	Val	Ala	Tyr	His	Leu	Cys	Lys
			180						185					190		
60	His	Leu	His	Ala	Glu	Gly	Ala	Lys	Leu	Ile	Val	Thr	Asp	Ile	Asn	Lys
		195						200					205			
65	Glu	Ala	Val	Gln	Arg	Ala	Val	Glu	Glu	Phe	Gly	Ala	Ser	Ala	Val	Glu
		210					215					220				
70	Pro	Asn	Glu	Ile	Tyr	Gly	Val	Glu	Cys	Asp	Ile	Tyr	Ala	Pro	Cys	Ala
	225					230					235					240

	Leu Gly Ala Thr Val Asn Asp Glu Thr Ile Pro Gln Leu Lys Ala Lys	
	245 250 255	
5	Val Ile Ala Gly Ser Ala Asn Asn Gln Leu Lys Glu Asp Arg His Gly	
	260 265 270	
10	Asp Ile Ile His Glu Met Gly Ile Val Tyr Ala Pro Asp Tyr Val Ile	
	275 280 285	
15	Asn Ala Gly Gly Val Ile Asn Val Ala Asp Glu Leu Tyr Gly Tyr Asn	
	290 295 300	
	Arg Glu Arg Ala Leu Lys Arg Val Glu Ser Ile Tyr Asp Thr Ile Ala	
	305 310 315 320	
20	Lys Val Ile Glu Ile Ser Lys Arg Asp Gly Ile Ala Thr Tyr Val Ala	
	325 330 335	
25	Ala Asp Arg Leu Ala Glu Glu Arg Ile Ala Ser Leu Lys Asn Ser Arg	
	340 345 350	
30	Ser Thr Tyr Leu Arg Asn Gly His Asp Ile Ile Ser Arg Arg	
	355 360 365	
35	<210> 7	
	<211> 1095	
	<212> DNA	
	<213> Candida boidinii	
40	<220>	
	<221> CDS	
	<222> (1)..(1095)	
	<223>	
45	<400> 7	
	atg aag att gtc tta gtt ctt tat gat gct ggt aag cac gct gct gat	48
	Met Lys Ile Val Leu Val Leu Tyr Asp Ala Gly Lys His Ala Ala Asp	
	1 5 10 15	
50	gaa gaa aaa tta tat ggt tct act gaa aat aaa tta ggt att gct aat	96
	Glu Glu Lys Leu Tyr Gly Ser Thr Glu Asn Lys Leu Gly Ile Ala Asn	
	20 25 30	
55	tgg tta aaa gat caa ggt cat gaa cta att act act tct gat aaa gaa	144
	Trp Leu Lys Asp Gln Gly His Glu Leu Ile Thr Thr Ser Asp Lys Glu	
	35 40 45	
	ggt gaa aca agt gaa ttg gat aaa cat atc cca gat gct gat att atc	192
	Gly Glu Thr Ser Glu Leu Asp Lys His Ile Pro Asp Ala Asp Ile Ile	
	50 55 60	

	atc acc act cct ttc cat cct gct tat atc act aag gaa aga ctt gac	240
	Ile Thr Thr Pro Phe His Pro Ala Tyr Ile Thr Lys Glu Arg Leu Asp	
	65 70 75 80	
5	aag gct aag aac tta aaa tta gtc gtt gtc gct ggt gtt ggt tct gat	288
	Lys Ala Lys Asn Leu Lys Leu Val Val Val Ala Gly Val Gly Ser Asp	
	85 90 95	
10	cac att gat tta gat tat att aat caa aca ggt aag aaa atc tca gtc	336
	His Ile Asp Leu Asp Tyr Ile Asn Gln Thr Gly Lys Lys Ile Ser Val	
	100 105 110	
15	ctg gaa gtt aca ggt tct aat gtt gtc tct gtt gct gaa cac gtt gtc	384
	Leu Glu Val Thr Gly Ser Asn Val Val Ser Val Ala Glu His Val Val	
	115 120 125	
20	atg acc atg ctt gtc ttg gtt aga aat ttc gtt cca gca cat gaa caa	432
	Met Thr Met Leu Val Leu Val Arg Asn Phe Val Pro Ala His Glu Gln	
	130 135 140	
25	att att aac cac gat tgg gag gtt gct gct atc gct aag gat gct tac	480
	Ile Ile Asn His Asp Trp Glu Val Ala Ala Ile Ala Lys Asp Ala Tyr	
	145 150 155 160	
30	gat atc gaa ggt aaa act atc gct acc att ggt gct ggt aga att ggt	528
	Asp Ile Glu Gly Lys Thr Ile Ala Thr Ile Gly Ala Gly Arg Ile Gly	
	165 170 175	
35	tac aga gtc ttg gaa aga tta ctg cca ttt aat cca aaa gaa tta tta	576
	Tyr Arg Val Leu Glu Arg Leu Leu Pro Phe Asn Pro Lys Glu Leu Leu	
	180 185 190	
40	tac tac gat tat caa gct tta cca aaa gaa gct gaa gaa aaa gtt ggt	624
	Tyr Tyr Asp Tyr Gln Ala Leu Pro Lys Glu Ala Glu Glu Lys Val Gly	
	195 200 205	
45	gct aga aga gtt gaa aat att gaa gaa tta gtt gct caa gct gat atc	672
	Ala Arg Arg Val Glu Asn Ile Glu Glu Leu Val Ala Gln Ala Asp Ile	
	210 215 220	
50	gtt aca gtt aat gct cca tta cac gca ggt aca aaa ggt tta att aat	720
	Val Thr Val Asn Ala Pro Leu His Ala Gly Thr Lys Gly Leu Ile Asn	
	225 230 235 240	
55	aag gaa tta tta tct aaa ttt aaa aaa ggt gct tgg tta gtc aat acc	768
	Lys Glu Leu Leu Ser Lys Phe Lys Lys Gly Ala Trp Leu Val Asn Thr	
	245 250 255	
60	gca aga ggt gct att gct gtt gct gaa gat gtt gca gca gct tta gaa	816
	Ala Arg Gly Ala Ile Ala Val Ala Glu Asp Val Ala Ala Ala Leu Glu	
	260 265 270	
65	tct ggt caa tta aga ggt tac ggt ggt gat gtt tgg ttc cca caa cca	864
	Ser Gly Gln Leu Arg Gly Tyr Gly Gly Asp Val Trp Phe Pro Gln Pro	
	275 280 285	
70	gct cca aag gat cac cca tgg aga gat atg aga aat aaa tat ggt gct	912
	Ala Pro Lys Asp His Pro Trp Arg Asp Met Arg Asn Lys Tyr Gly Ala	
	290 295 300	

	ggt	aat	gcc	atg	act	cct	cac	tac	tct	ggt	act	act	tta	gac	gct	caa	960
	Gly	Asn	Ala	Met	Thr	Pro	His	Tyr	Ser	Gly	Thr	Thr	Leu	Asp	Ala	Gln	
	305					310					315					320	
5	aca	aga	tac	gct	gaa	ggt	act	aaa	aat	att	ttg	gaa	tca	ttc	ttt	acc	1008
	Thr	Arg	Tyr	Ala	Glu	Gly	Thr	Lys	Asn	Ile	Leu	Glu	Ser	Phe	Phe	Thr	
				325						330					335		
10	ggt	aaa	ttt	gat	tac	aga	cca	caa	gat	att	atc	tta	tta	aat	ggt	gaa	1056
	Gly	Lys	Phe	Asp	Tyr	Arg	Pro	Gln	Asp	Ile	Ile	Leu	Leu	Asn	Gly	Glu	
			340						345					350			
15	tac	ggt	act	aaa	gct	tac	ggt	aaa	cac	gat	aag	aaa	taa				1095
	Tyr	Val	Thr	Lys	Ala	Tyr	Gly	Lys	His	Asp	Lys	Lys					
		355						360									
20	<210>	8															
	<211>	364															
	<212>	PRT															
	<213>	Candida boidinii															
25	<400>	8															
	Met	Lys	Ile	Val	Leu	Val	Leu	Tyr	Asp	Ala	Gly	Lys	His	Ala	Ala	Asp	
	1			5						10					15		
30	Glu	Glu	Lys	Leu	Tyr	Gly	Ser	Thr	Glu	Asn	Lys	Leu	Gly	Ile	Ala	Asn	
			20						25					30			
35	Trp	Leu	Lys	Asp	Gln	Gly	His	Glu	Leu	Ile	Thr	Thr	Ser	Asp	Lys	Glu	
		35						40					45				
40	Gly	Glu	Thr	Ser	Glu	Leu	Asp	Lys	His	Ile	Pro	Asp	Ala	Asp	Ile	Ile	
	50						55					60					
45	Ile	Thr	Thr	Pro	Phe	His	Pro	Ala	Tyr	Ile	Thr	Lys	Glu	Arg	Leu	Asp	
	65				70						75					80	
50	Lys	Ala	Lys	Asn	Leu	Lys	Leu	Val	Val	Val	Ala	Gly	Val	Gly	Ser	Asp	
				85						90					95		
55	His	Ile	Asp	Leu	Asp	Tyr	Ile	Asn	Gln	Thr	Gly	Lys	Lys	Ile	Ser	Val	
			100						105					110			
60	Leu	Glu	Val	Thr	Gly	Ser	Asn	Val	Val	Ser	Val	Ala	Glu	His	Val	Val	
		115						120					125				
65	Met	Thr	Met	Leu	Val	Leu	Val	Arg	Asn	Phe	Val	Pro	Ala	His	Glu	Gln	
	130						135					140					

5	Ile 145	Ile	Asn	His	Asp	Trp 150	Glu	Val	Ala	Ala	Ile 155	Ala	Lys	Asp	Ala	Tyr 160
10	Asp	Ile	Glu	Gly	Lys 165	Thr	Ile	Ala	Thr	Ile 170	Gly	Ala	Gly	Arg	Ile 175	Gly
15	Tyr	Arg	Val	Leu 180	Glu	Arg	Leu	Leu	Pro 185	Phe	Asn	Pro	Lys	Glu 190	Leu	Leu
20	Tyr	Tyr	Asp 195	Tyr	Gln	Ala	Leu	Pro 200	Lys	Glu	Ala	Glu	Glu 205	Lys	Val	Gly
25	Ala	Arg 210	Arg	Val	Glu	Asn	Ile 215	Glu	Glu	Leu	Val	Ala 220	Gln	Ala	Asp	Ile
30	Val 225	Thr	Val	Asn	Ala	Pro 230	Leu	His	Ala	Gly	Thr 235	Lys	Gly	Leu	Ile	Asn 240
35	Lys	Glu	Leu	Leu	Ser 245	Lys	Phe	Lys	Lys	Gly 250	Ala	Trp	Leu	Val	Asn 255	Thr
40	Ala	Arg	Gly	Ala 260	Ile	Ala	Val	Ala	Glu 265	Asp	Val	Ala	Ala 270	Ala	Leu	Glu
45	Ser	Gly	Gln 275	Leu	Arg	Gly	Tyr	Gly 280	Gly	Asp	Val	Trp	Phe 285	Pro	Gln	Pro
50	Ala	Pro 290	Lys	Asp	His	Pro	Trp 295	Arg	Asp	Met	Arg	Asn 300	Lys	Tyr	Gly	Ala
55	Gly 305	Asn	Ala	Met	Thr	Pro 310	His	Tyr	Ser	Gly	Thr 315	Thr	Leu	Asp	Ala	Gln 320
60	Thr	Arg	Tyr	Ala	Glu 325	Gly	Thr	Lys	Asn	Ile 330	Leu	Glu	Ser	Phe	Phe 335	Thr
65	Gly	Lys	Phe	Asp 340	Tyr	Arg	Pro	Gln	Asp 345	Ile	Ile	Leu	Leu	Asn 350	Gly	Glu
70	Tyr	Val	Thr 355	Lys	Ala	Tyr	Gly	Lys 360	His	Asp	Lys	Lys				



<211> 5686  
 <212> DNA  
 <213> Artificial

5 <220>  
 <223> Plasmid pAM3.25

<400> 9  
 10 tatgaagatt gtcttagttc tttatgatgc tggtaagcac gctgctgatg aagaaaaatt 60  
 atatggttct actgaaaata aattaggtat tgctaattgg ttaaaagatc aaggatcatga 120  
 actaattact acttctgata aagaaggatga aacaagtga ttggataaac atatcccaga 180  
 15 tgctgatatt atcatcacca ctcttttcca tcctgcttat atcactaagg aaagacttga 240  
 caaggctaag aacttaaaat tagtcgttgt cgctgggtgtt ggttctgatc acattgattt 300  
 agattatatt aatcaaacag gtaagaaaat ctgagtcctg gaagttacag gttctaattgt 360  
 20 tgtctctgtt gctgaacacg ttgtcatgac catgcttgct ttgggttagaa atttcgttcc 420  
 agcacatgaa caaattatta accacgattg ggagggttgct gctatcgcta aggatgctta 480  
 25 cgatatcgaa ggtaaaacta tcgctaccat tgggtgctggt agaattgggt acagagtctt 540  
 ggaaagatta ctcccattta atccaaaaga attattatac tacgattatc aagctttacc 600  
 aaaagaagct gaagaaaaag ttggtgctag aagagttgaa aatattgaag aattagttgc 660  
 30 tcaagctgat atcggttacag ttaatgctcc attacacgca ggtacaaaag gtttaattaa 720  
 taaggaatta ttatctaaat ttaaaaaagg tgcttggtta gtcaataccg caagaggtgc 780  
 35 tattgctgtt gctgaagatg ttgcagcagc tttagaatct ggtcaattaa gaggttacgg 840  
 tgggtgatgtt tgggtcccac aaccagctcc aaaggatcac ccatggagag atatgagaaa 900  
 taaatatggt gctggtaatg ccatgactcc tcaactactct ggtactactt tagacgctca 960  
 40 aacaagatac gctgaaggta ctaaaaatat tttggaatca ttctttaccg gtaaatttga 1020  
 ttacagacca caagatatta tcttattaaa tgggtgaatac gttactaaag cttacggtaa 1080  
 45 acacgataag aaataagacg tcaagcttgg ctgttttggc ggatgagaga agattttcag 1140  
 cctgatacag attaaatcag aacgcagaag cggctctgata aaacagaatt tgcttggcgg 1200  
 cagtagcgcg gtgggtccac ctgaccccat gccgaactca gaagtgaac gccgtagcgc 1260  
 50 cgatggtagt gtgggggtctc cccatgcgag agtagggaac tgccaggcat caaataaaac 1320  
 gaaaggctca gtcgaaagac tgggcctttc gttttatctg ttgtttgtcg gtgaacgctc 1380  
 55 tcctgagtag gacaaatccg cggggagcgg atttgaacgt tgcaagcaa cggcccggag 1440  
 ggtggcgggc aggacgcccg ccataaactg ccaggcatca aattaagcag aaggccatcc 1500  
 tgacggatgg cttttttgcg tttctacaaa ctcttttgtt tatttttcta aatacattca 1560

	aatatgtatc cgctcatgag acaataaccc tgataaatgc ttcaataata ttgaaaaagg	1620
5	aagagtatga gtattcaaca tttccgtgtc gcccttattc ccttttttgc ggcattttgc	1680
	cttcctgttt ttgctcacc agaaacgctg gtgaaagtaa aagatgctga agatcagttg	1740
	ggtgcacgag tgggttacat cgaactggat ctcaacagcg gtaagatcct tgagagtttt	1800
10	cgccccgaag aacgttttcc aatgatgagc acttttaaaag ttctgctatg tggcgcggtg	1860
	ttatcccgtg ttgacgccgg gcaagagcaa ctcggtcgcc gcatacacta ttctcagaat	1920
15	gacttggttg agtactcacc agtcacagaa aagcatctta cggatggcat gacagtaaga	1980
	gaattatgca gtgctgccat aaccatgagt gataaactg cggccaactt acttctgaca	2040
	acgatcggag gaccgaagga gctaaccgct tttttgcaca acatggggga tcatgtaact	2100
20	cgccttgatc gttgggaacc ggagctgaat gaagccatac caaacgacga gcgtgacacc	2160
	acgatgcctg tagcaatggc aacaacgttg cgcaaactat taactggcga actacttact	2220
25	ctagcttccc ggcaacaatt aatagactgg atggaggcgg ataaagttgc aggaccactt	2280
	ctgcgctcgg cccttccggc tggctggttt attgctgata aatctggagc cgggtgagcgt	2340
	gggtctcgcg gtatcattgc agcactgggg ccagatggta agccctcccg tatcgtagtt	2400
30	atctacacga cggggagtca ggcaactatg gatgaacgaa atagacagat cgctgagata	2460
	ggtgcctcac tgattaagca ttggtaactg tcagaccaag tttactcata tatacttttag	2520
35	attgatttaa aacttcattt ttaatttaaa aggatctagg tgaagatcct ttttgataat	2580
	ctcatgacca aaatccctta acgtgagttt tcgttccact gagcgtcaga ccccgtagaa	2640
	aagatcaaag gatcttcttg agatcctttt tttctgcgcg taatctgctg cttgcaaaca	2700
40	aaaaaaccac cgctaccagc ggtggtttgt ttgccggatc aagagctacc aactcctttt	2760
	ccgaaggtaa ctggcttcag cagagcgcag ataccaaata ctgtccttct agtgtagccg	2820
45	tagttaggcc accacttcaa gaactctgta gcaccgccta catacctcgc tctgctaata	2880
	ctgttaccag tggctgctgc cagtggcgat aagtcgtgtc ttaccggggt ggactcaaga	2940
	cgatagttac cggataaggc gcagcggctg ggctgaacgg ggggttcgtg cacacagccc	3000
50	agcttgagc gaacgaccta caccgaactg agatacctac agcgtgagct atgagaaagc	3060
	gccacgcttc ccgaaggag aaaggcggac aggtatccgg taagcggcag ggtcggaaaca	3120
55	ggagagcgca cgaggagct tccaggggga aacgcctggg atctttatag tcctgtcggg	3180
	tttcgccacc tctgacttga gcgtcgattt ttgtgatgct cgtcaggggg gcggagccta	3240
	tggaaaaacg ccagcaacgc ggctttttta cggttcctgg ccttttgctg gccttttgct	3300

	cacatgttct	ttcctgcgtt	atccctgat	tctgtggata	accgtattac	cgcttttgag	3360
	tgagctgata	ccgctcgccg	cagccgaacg	accgagcgca	gcgagtcagt	gagcgaggaa	3420
5	gcggaagagc	gcctgatgcg	gtattttctc	cttacgcatac	tgtgcggtat	ttcacaccgc	3480
	atatatggtg	cactctcagt	acaatctgct	ctgatgccgc	atagttaagc	cagtatacac	3540
10	tccgctatcg	ctacgtgact	gggtcatggc	tgcgccccga	cacccgcaa	cacccgctga	3600
	cgcgccctga	cgggcttgct	tgctcccggc	atccgcttac	agacaagctg	tgaccgtctc	3660
	cgggagctgc	atgtgtcaga	ggttttcacc	gtcatcaccg	aaacgcgcga	ggcagctgcg	3720
15	gtaaagctca	tcagcgtggg	cgtgaagcga	ttcacagatg	tctgcctgtt	catccgcgtc	3780
	cagctcgttg	agttttctca	gaagcgttaa	tgtctggctt	ctgataaagc	gggccatgtt	3840
20	aagggcggtt	ttttcctgtt	tggtcacttg	atgcctccgt	gtaaggggga	atttctgttc	3900
	atgggggtaa	tgataccgat	gaaacgagag	aggatgctca	cgatacgggt	tactgatgat	3960
	gaacatgccc	ggttactgga	acgttgtgag	ggtaaacaac	tggcggtatg	gatgcggcgg	4020
25	gaccagagaa	aaatcactca	gggtcaatgc	cagcgcttcg	ttaatacaga	tgtaggtgtt	4080
	ccacagggta	gccagcagca	tcctgcgatg	cagatccgga	acataatggt	gcagggcgct	4140
30	gacttccgcg	tttccagact	ttacgaaaca	cggaaaccca	agaccattca	tgttggttgct	4200
	caggctgcag	acgttttgca	gcagcagtcg	cttcacgttc	gctcgcgtat	cggtgattca	4260
	ttctgctaac	cagtaaggca	accccgccag	cctagccggg	tcctcaacga	caggagcacg	4320
35	atcatgcgca	cccgtggcca	ggacccaacg	ctgcccagaga	tgcgcccgcg	gcggctgctg	4380
	gagatggcgg	acgcgatgga	tatgttctgc	caaggggttg	tttgcgcat	cacagtcttc	4440
40	cgcaagaatt	gattggctcc	aattcttggg	gtggtgaatc	cgttagcgag	gtgccgcccg	4500
	cttccattca	ggtcgaggtg	gcccggctcc	atgcaccgcg	acgcaacgcg	gggaggcaga	4560
	caaggtatag	ggcggcgcct	acaatccatg	ccaaccggtt	ccatgtgctc	gccgaggcgg	4620
45	cataaatcgc	cgtgacgatc	agcgggtccg	tgatcgaagt	taggctggta	agagccgcga	4680
	gcgatccttg	aagctgtccc	tgatggtcgt	catctacctg	cctggacagc	atggcctgca	4740
50	acgcgggcat	cccgatgccg	ccggaagcga	gaagaatcat	aatgggggaag	gccatccagc	4800
	ctcgcgtcgc	gaacgccagc	aagacgtagc	ccagcgcgtc	ggccgccatg	ccggcgataa	4860
	tggcctgctt	ctcgcggaaa	cgtttggtgg	cgggaccagt	gacgaaggct	tgagcgaggg	4920
55	cgtgcaagat	tccgaatacc	gcaagcgaca	ggccgatcat	cgtcgcgctc	cagcgaaagc	4980
	ggtcctcgcc	gaaaatgacc	cagagcgctg	ccggcacctg	tcctacgagt	tgcatgataa	5040
	agaagacagt	cataagtgcg	gcgacgatag	tcatgccccg	cgcccaccgg	aaggagctga	5100

ctggggttgaa ggctctcaag ggcatcggtc gacgctctcc cttatgcgac tcctgcatta 5160  
 5 ggaagcagcc cagtagtagg ttgaggccgt tgagcaccgc cgccgcaagg aatggtgcat 5220  
 gctcgatggc tacgagggca gacagtaagt ggatttacca taatccctta attgtacgca 5280  
 ccgctaaaac gcgttcagcg cgatcacggc agcagacagg taaaaatggc aacaaaccac 5340  
 10 cctaaaaact gcgcgatcgc gcctgataaa ttttaaccgt atgaatacct atgcaaccag 5400  
 aggggtacagg ccacattacc ccacttaat ccactgaagc tgccattttt catgggtttca 5460  
 15 ccatcccagc gaagggccat gcatgcatcg aaattaatac gacgaaatta atacgactca 5520  
 ctatagggca attgcgatca ccacaattca gcaaattgtg aacatcatca cgttcattctt 5580  
 tccctgggttg ccaatggccc attttcctgt cagtaacgag aaggtcgcga attcaggcgc 5640  
 20 tttttagact ggtcgtaatg aacaattctt aagaaggaga tataca 5686

<210> 10  
 <211> 5106  
 25 <212> DNA  
 <213> Artificial

<220>  
 <223> Plasmid pAM10.1  
 30

<400> 10  
 gaaggagata tacatatgac attagaaatc ttcgaatact tagaaaaata tgattatgag 60  
 35 caagtagtat tttgtcaaga taaagaatct ggtttaaaag caattattgc aattcatgat 120  
 acaacacttg gaccggctct tgggtgaaca agaatgtgga catatgattc tgaagaagcg 180  
 gcgattgaag atgcattgcy tcttgcaaaa gggatgacat acaaaaaacgc agcagctggg 240  
 40 ttaaaacttag gtggtgcgaa aacagtaatt atcggtgatc ctcgtaaaga taagagcgaa 300  
 gcaatgttcc gtgcactagg acgttatatc caaggactaa acggacgtta cattacagct 360  
 45 gaagatgttg gtacaacagt agatgatatg gatattatcc atgaagaaac tgactttgta 420  
 acaggatatct caccatcatt cggttcttct ggtaacccat ctccggtaac tgcatacggg 480  
 gtttaccgtg gtatgaaagc agctgcaaaa gaagctttcg gtactgacaa tttagaagga 540  
 50 aaagtaattg ctgttcaagg cgttggtaac gtagcatatc acctatgcaa acatttacac 600  
 gctgaaggag caaaattaat tgttacagat attaataaag aagctgtaca acgtgctgta 660  
 55 gaagaattcg gtgcatcagc agttgaacca aatgaaattt acgggtgttg atgcgatatt 720  
 tacgcaccat gtgcactagg cgcaacagtt aatgatgaaa ctattccaca acttaaagca 780  
 aaagtaatcg caggttctgc gaataaccaa ttaaaagaag atcgtcatgg tgacatcatt 840

	catgaaatgg	gtattgtata	cgcaccagat	tatgtaatta	atgcagggtgg	cgtaattaac	900
	gtagcagacg	aattatatgg	atacaataga	gaacgtgcac	taaaacgtgt	tgagtctatt	960
5	tatgacacga	ttgcaaaagt	aatcgaaatt	tcaaaacgcg	atggcatagc	aacttatgta	1020
	gcggcagatc	gtctagctga	agagcgcatt	gcaagcttga	agaattctcg	tagcacttac	1080
	ttacgcaacg	gtcacgatat	tattagccgt	cgctaacgcg	tttgcggttg	gcaaaatggc	1140
10	gcagcagcaa	ggcgtggcgg	tgaaaacctc	tgccgaagcc	ctgcaacagg	ccattgacga	1200
	taatttctgg	caagccgaat	accgcgacta	ccgccgtacc	tccatctaaa	agcttatcga	1260
15	tgataagctg	tcaaacaatga	gaattacaac	ttatatcgta	tggggctgac	ttcagggtgct	1320
	acatttgaag	agataaattg	cactgaaatc	tagaaatatt	ttatctgatt	aataagatga	1380
	tcttcttgag	atcgtttttg	tctgcgcgta	atctcttgct	ctgaaaacga	aaaaaccgcc	1440
20	ttgcagggcg	gtttttcgaa	ggttctctga	gctaccaact	ctttgaaccg	aggtaactgg	1500
	cttggaggag	cgcagtcacc	aaaacttgtc	ctttcagttt	agccttaacc	ggcgcgatgac	1560
25	ttcaagacta	actcctctaa	atcaattacc	agtggctgct	gccagtggtg	cttttgcatg	1620
	tctttccggg	ttggactcaa	gacgatagtt	accggataag	gcgcagcggg	cggactgaac	1680
	gggggggttcg	tgcatacagt	ccagcttggg	gcgaactgcc	tacccggaac	tgagtgtcag	1740
30	gcgtggaatg	agacaaacgc	ggccataaca	gcggaatgac	accggtaaac	cgaaaggcag	1800
	gaacaggaga	gcgcacgagg	gagccgccag	gggaaacgcc	tggtatcttt	atagtcctgt	1860
35	cggggtttcgc	caccactgat	ttgagcgtca	gatttcgtga	tgcttgtcag	gggggcggag	1920
	cctatggaaa	aacggctttg	ccgcggccct	ctcacttccc	tgtaaagtat	cttcctggca	1980
	tcttccagga	aatctccgcc	ccgttcgtaa	gccatttccg	ctcgccgcag	tcgaacgacc	2040
40	gagcgtagcg	agtcagtga	cgaggaagcg	gaatatatcc	tgtatcacat	attctgctga	2100
	cgcaccgggtg	cagccttttt	tctcctgcca	catgaagcac	ttcactgaca	ccctcatcag	2160
45	tgccaacata	gtaagccagt	atacactccg	ctagcgcgtga	tgtccggcgg	tgcttttgcc	2220
	gttacgcacc	accccgctcag	tagctgaaca	ggaggggacag	ctgatagaaa	cagaagccac	2280
	tggagcacct	caaaaaacacc	atcatacact	aaatcagtaa	gttggcagca	tcacccgacg	2340
50	cactttgcgc	cgaataaata	cctgtgacgg	aagatcactt	cgcagaataa	ataaatcctg	2400
	gtgtccctgt	tgataccggg	aagccctggg	ccaacttttg	gcgaaaatga	gacgttgatc	2460
55	ggcacgtaag	aggttccaac	tttcaccata	atgaaataag	atcactaccg	ggcgtatttt	2520
	ttgagttatc	gagattttca	ggagctaagg	aagctaaaat	ggagaaaaaa	atcactggat	2580
	ataccaccgt	tgatatatcc	caatggcatc	gtaaagaaca	ttttgaggca	tttcagtcag	2640

	ttgctcaatg tacctataac cagaccgttc agctggatat tacggccttt ttaaagaccg	2700
5	taaagaaaaa taagcacaag ttttatccgg cctttattca cattcttgcc cgctgatga	2760
	atgctcatcc ggaattccgt atggcaatga aagacgggtga gctggtgata tgggatagtg	2820
	ttcacccttg ttacaccgtt ttccatgagc aaactgaaac gttttcatcg ctctggagtg	2880
10	aataccacga cgatttccgg cagtttctac acatatattc gcaagatgtg gcgtgttacg	2940
	gtgaaaacct ggcctatttc cctaaagggt ttattgagaa tatgtttttc gtctcagcca	3000
15	atccctgggt gagtttcacc agttttgatt taaacgtggc caatatggac aacttcttcg	3060
	ccccggtttt caccatgggc aaatattata cgcaaggcga caagggtgctg atgccgctgg	3120
	cgattcaggt tcatcatgcc gtctgtgatg gcttccatgt cggcagaatg cttaatgaat	3180
20	tacaacagta ctgcatgag tggcagggcg gggcgtaatt tttttaaggc agttattggt	3240
	gcccttaaac gcctgggtgct acgcctgaat aagtataat aagcggatga atggcagaaa	3300
25	ttcgaaagca aattcgaccc ggtcgtcgggt tcagggcagg gtcgttaaat agccgcttat	3360
	gtctattgct ggtttaccgg tttattgact accggaagca gtgtgaccgt gtgcttctca	3420
	aatgcctgag gccagtttgc tcaggctctc cccgtggagg taataattga cgatatgac	3480
30	atattattctg cctcccagag cctgataaaa acggttagcg cttcgtaat acagatgtag	3540
	gtgttccaca gggtagccag cagcatcctg cgatgcagat ccggaacata atgggtgcagg	3600
35	gcgcttgttt cggcgtgggt atgggtggcag gcccgtggc cgggggactg ttgggcgctg	3660
	ccggcacctg tcctacgagt tgcattgataa agaagacagt cataagtgcg gcgacgatag	3720
	tcatgccccg cgcccaccgg aaggagctac cggacagcgg tgccgactgt tgtaactcag	3780
40	aataagaaat gaggccgctc atggcggtga ctctcagtca tagtatcgtg gtatcaccgg	3840
	ttgggtccac tctctgttgc gggcaacttc agcagcacgt aggggacttc cgcgtttcca	3900
45	gactttacga aacacggaac ccgaagacca ttcatgttgt tgctcaggtc gcagacgttt	3960
	tgcagcagca gtgcgttcac gttcgtctgc gtatcgggtga ttcatcttgc taaccagtaa	4020
	ggcaaccccc ccagcctagc cgggtcctca acgacaggag cacgatcatg cgcaccctg	4080
50	gccaggaccc aacgctgccc gagatgcgcc gcgtgcggct gctggagatg gcggacgcga	4140
	tggatatgtt ctgccaaagg ttggtttgct cattcacagt tctccgcaag aattgattgg	4200
55	ctccaattct tggagtgggt aatccgttag cgaggtgccg ccggcttcca ttcaggtcga	4260
	ggtggccccg ctccatgcac cgcgacgcaa cgcggggagg cagacaagggt atagggcggc	4320
	gcctacaatc catgccaacc cgttccatgt gctcgccgag gcggcataaa tcgccgtgac	4380

gatcagcggg ccagtgatcg aagttaggct ggtaagagcc gcgagcgatc cttgaagctg 4440  
 tccctgatgg tcgtcatcta cctgcctgga cagcatggcc tgcaacgcgg gcatcccgat 4500  
 5 gccgccggaa gcgagaagaa tcataatggg gaaggccatc cagcctcgcg tcgcgaacgc 4560  
 cagcaagacg tagcccagcg cgtcggccgc catgccggcg ataatggcct gcttctcgcc 4620  
 10 gaaacgtttg gtggcgggac cagtgaagaa ggcttgagcg agggcgtgca agattccgaa 4680  
 taccgcaagc gacaggccga tcatcgtcgc gctccagcga aagcggtcct cgccgaaaat 4740  
 gacccagagc gctgccggca cctgtcctac gagttgcatg ataaagaaga cagtcataag 4800  
 15 tgcggcgacg atagtcatgc cccgcgcccc ccggaaggag ctgactgggt tgaaggctct 4860  
 caagggcatc ggtcgacgct ctcccttatg cgactcctgc attaggaagc agcccagtag 4920  
 taggttgagg ccgttgagca ccgccgccgc aaggaatggg gcatgcatcg atcaccacaa 4980  
 20 ttcagcaaata tgtgaacatc atcacgttca tctttccctg gttgccaatg gccattttc 5040  
 ctgtcagtaa cgagaaggtc gcgaattcag gcgcttttta gactggtcgt aatgaacaat 5100  
 25 tcttaa 5106

<210> 11  
 <211> 5597  
 30 <212> DNA  
 <213> Unknown

<220>  
 <223> Plasmid  
 35  
 <220>  
 <221> CDS  
 <222> (25)..(1749)  
 <223> scfA - malic enzyme gene  
 40

<400> 11  
 aattcttaag aaggagatat acat atg gat att caa aaa aga gtg agt gac 51  
 45 Met Asp Ile Gln Lys Arg Val Ser Asp  
 1 5  
 atg gaa cca aaa aca aaa aaa cag cgt tcg ctt tat atc cct tac gct 99  
 Met Glu Pro Lys Thr Lys Lys Gln Arg Ser Leu Tyr Ile Pro Tyr Ala  
 10 15 20 25  
 50 ggc cct gta ctg ctg gaa ttt ccg ttg ttg aat aaa ggc agt gcc ttc 147  
 Gly Pro Val Leu Leu Glu Phe Pro Leu Leu Asn Lys Gly Ser Ala Phe  
 30 35 40  
 55 agc atg gaa gaa cgc cgt aac ttc aac ctg ctg ggg tta ctg ccg gaa 195  
 Ser Met Glu Glu Arg Arg Asn Phe Asn Leu Leu Gly Leu Leu Pro Glu  
 45 50 55  
 gtg gtc gaa acc atc gaa gaa caa gcg gaa cga gca tgg atc cag tat 243

	Val	Val	Glu	Thr	Ile	Glu	Glu	Gln	Ala	Glu	Arg	Ala	Trp	Ile	Gln	Tyr	
			60					65					70				
5	cag	gga	ttc	aaa	acc	gaa	atc	gac	aaa	cac	atc	tac	ctg	cgt	aac	atc	291
	Gln	Gly	Phe	Lys	Thr	Glu	Ile	Asp	Lys	His	Ile	Tyr	Leu	Arg	Asn	Ile	
		75					80					85					
10	cag	gac	act	aac	gaa	acc	ctc	ttc	tac	cgt	ctg	gta	aac	aat	cat	ctt	339
	Gln	Asp	Thr	Asn	Glu	Thr	Leu	Phe	Tyr	Arg	Leu	Val	Asn	Asn	His	Leu	
	90				95						100					105	
15	gat	gag	atg	atg	cct	gtt	att	tat	acc	cca	acc	gtc	ggc	gca	gcc	tgt	387
	Asp	Glu	Met	Met	Pro	Val	Ile	Tyr	Thr	Pro	Thr	Val	Gly	Ala	Ala	Cys	
					110					115					120		
	gag	cgt	ttt	tct	gag	atc	tac	cgc	cgt	tca	cgc	ggc	gtg	ttt	atc	tct	435
	Glu	Arg	Phe	Ser	Glu	Ile	Tyr	Arg	Arg	Ser	Arg	Gly	Val	Phe	Ile	Ser	
				125				130						135			
20	tac	cag	aac	cgg	cac	aat	atg	gac	gat	att	ctg	caa	aac	gtg	ccg	aac	483
	Tyr	Gln	Asn	Arg	His	Asn	Met	Asp	Asp	Ile	Leu	Gln	Asn	Val	Pro	Asn	
			140					145					150				
25	cat	aat	att	aaa	gtg	att	gtg	gtg	act	gac	ggc	gaa	cgc	att	ctg	ggg	531
	His	Asn	Ile	Lys	Val	Ile	Val	Val	Thr	Asp	Gly	Glu	Arg	Ile	Leu	Gly	
		155					160					165					
30	ctt	ggc	gac	cag	ggc	atc	ggc	ggg	atg	ggc	att	ccg	atc	ggc	aaa	ctg	579
	Leu	Gly	Asp	Gln	Gly	Ile	Gly	Gly	Met	Gly	Ile	Pro	Ile	Gly	Lys	Leu	
	170					175					180					185	
35	tcg	ctc	tat	acc	gcc	tgt	ggc	ggc	atc	agc	ccg	gcg	tat	acc	ctt	ccg	627
	Ser	Leu	Tyr	Thr	Ala	Cys	Gly	Gly	Ile	Ser	Pro	Ala	Tyr	Thr	Leu	Pro	
					190					195					200		
	gtg	gtg	ctg	gat	gtc	gga	acg	aac	aac	caa	cag	ctg	ctt	aac	gat	ccg	675
	Val	Val	Leu	Asp	Val	Gly	Thr	Asn	Asn	Gln	Gln	Leu	Leu	Asn	Asp	Pro	
				205					210					215			
40	ctg	tat	atg	ggc	tgg	cgt	aat	ccg	cgt	atc	act	gac	gac	gaa	tac	tat	723
	Leu	Tyr	Met	Gly	Trp	Arg	Asn	Pro	Arg	Ile	Thr	Asp	Asp	Glu	Tyr	Tyr	
			220					225					230				
45	gaa	ttc	gtt	gat	gaa	ttt	atc	cag	gct	gtg	aaa	caa	cgc	tgg	cca	gac	771
	Glu	Phe	Val	Asp	Glu	Phe	Ile	Gln	Ala	Val	Lys	Gln	Arg	Trp	Pro	Asp	
		235					240					245					
50	gtg	ctg	ttg	cag	ttt	gaa	gac	ttt	gct	caa	aaa	aat	gcg	atg	ccg	tta	819
	Val	Leu	Leu	Gln	Phe	Glu	Asp	Phe	Ala	Gln	Lys	Asn	Ala	Met	Pro	Leu	
	250					255					260					265	
55	ctt	aac	cgc	tat	cgc	aat	gaa	att	tgt	tct	ttt	aac	gat	gac	att	cag	867
	Leu	Asn	Arg	Tyr	Arg	Asn	Glu	Ile	Cys	Ser	Phe	Asn	Asp	Asp	Ile	Gln	
					270					275					280		
	ggc	act	gcg	gcg	gta	aca	gtc	ggc	aca	ctg	atc	gca	gca	agc	cgc	gcg	915
	Gly	Thr	Ala	Ala	Val	Thr	Val	Gly	Thr	Leu	Ile	Ala	Ala	Ser	Arg	Ala	
				285					290					295			



		gca ggt ggt cag tta agc gag aaa aaa atc gtc ttc ctt ggc gca ggt	963
		Ala Gly Gly Gln Leu Ser Glu Lys Lys Ile Val Phe Leu Gly Ala Gly	
		300 305 310	
5		tca gcg gga tgc ggc att gcc gaa atg atc atc tcc cag acc cag cgc	1011
		Ser Ala Gly Cys Gly Ile Ala Glu Met Ile Ile Ser Gln Thr Gln Arg	
		315 320 325	
10		gaa gga tta agc gag gaa gcg gcg cgg cag aaa gtc ttt atg gtc gat	1059
		Glu Gly Leu Ser Glu Glu Ala Ala Arg Gln Lys Val Phe Met Val Asp	
		330 335 340 345	
15		cgc ttt ggc ttg ctg act gac aag atg ccg aac ctg ctg cct ttc cag	1107
		Arg Phe Gly Leu Leu Thr Asp Lys Met Pro Asn Leu Leu Pro Phe Gln	
		350 355 360	
		acc aaa ctg gtg cag aag cgc gaa aac ctc agt gac tgg gat acc gac	1155
		Thr Lys Leu Val Gln Lys Arg Glu Asn Leu Ser Asp Trp Asp Thr Asp	
		365 370 375	
20		agc gat gtg ctg tca ctg ctg gat gtg gtg cgc aat gta aaa cca gat	1203
		Ser Asp Val Leu Ser Leu Leu Asp Val Val Arg Asn Val Lys Pro Asp	
		380 385 390	
25		att ctg att ggc gtc tca gga cag acc ggg ctg ttt acg gaa gag atc	1251
		Ile Leu Ile Gly Val Ser Gly Gln Thr Gly Leu Phe Thr Glu Glu Ile	
		395 400 405	
30		atc cgt gag atg cat aaa cac tgt ccg cgt ccg atc gtg atg ccg ctg	1299
		Ile Arg Glu Met His Lys His Cys Pro Arg Pro Ile Val Met Pro Leu	
		410 415 420 425	
35		tct aac ccg acg tca cgc gtg gaa gcc aca ccg cag gac att atc gcc	1347
		Ser Asn Pro Thr Ser Arg Val Glu Ala Thr Pro Gln Asp Ile Ile Ala	
		430 435 440	
		tgg acc gaa ggt aac gcg ctg gtc gcc acg ggc agc ccg ttt aat cca	1395
		Trp Thr Glu Gly Asn Ala Leu Val Ala Thr Gly Ser Pro Phe Asn Pro	
		445 450 455	
40		gtg gta tgg aaa gat aaa atc tac cct atc gcc cag tgt aac aac gcc	1443
		Val Val Trp Lys Asp Lys Ile Tyr Pro Ile Ala Gln Cys Asn Asn Ala	
		460 465 470	
45		ttt att ttc ccg ggc atc ggc ctg ggt gtt att gct tcc ggc gcg tca	1491
		Phe Ile Phe Pro Gly Ile Gly Leu Gly Val Ile Ala Ser Gly Ala Ser	
		475 480 485	
50		cgt atc acc gat gag atg ctg atg tcg gca agt gaa acg ctg gcg cag	1539
		Arg Ile Thr Asp Glu Met Leu Met Ser Ala Ser Glu Thr Leu Ala Gln	
		490 495 500 505	
55		tat tca cca ttg gtg ctg aac ggc gaa ggt atg gta ctg ccg gaa ctg	1587
		Tyr Ser Pro Leu Leu Asn Gly Glu Gly Met Val Leu Pro Glu Leu	
		510 515 520	
		aaa gat att cag aaa gtc tcc cgc gca att gcg ttt gcg gtt ggc aaa	1635
		Lys Asp Ile Gln Lys Val Ser Arg Ala Ile Ala Phe Ala Val Gly Lys	
		525 530 535	

	atg gcg cag cag caa ggc gtg gcg gtg aaa acc tct gcc gaa gcc ctg	1683
	Met Ala Gln Gln Gln Gly Val Ala Val Lys Thr Ser Ala Glu Ala Leu	
	540 545 550	
5	caa cag gcc att gac gat aat ttc tgg caa gcc gaa tac cgc gac tac	1731
	Gln Gln Ala Ile Asp Asp Asn Phe Trp Gln Ala Glu Tyr Arg Asp Tyr	
	555 560 565	
10	cgc cgt acc tcc atc taa aagcttatcg atgataagct gtcaaactg	1779
	Arg Arg Thr Ser Ile	
	570	
15	agaattacaa cttatatcgt atggggctga cttcaggtgc tacatttgaa gagataaatt	1839
	gcactgaaat ctagaaatat tttatctgat taataagatg atcttcttga gatcgttttg	1899
	gtctgcgcgt aatctcttgc tctgaaaacg aaaaaaccgc cttgcagggc ggtttttcga	1959
20	aggttctctg agctaccaac tctttgaacc gaggtaactg gcttggagga gcgcagtcac	2019
	caaaacttgt cctttcagtt tagccttaac cggcgcacga cttcaagact aactcctcta	2079
25	aatcaattac cagtggctgc tgccagtggg gcttttgcac gtctttccgg gttggactca	2139
	agacgatagt taccggataa ggcgcagcgg tcggactgaa cgggggggttc gtgcatacag	2199
	tccagcttgg agcgaactgc ctaccgggaa ctgagtgtca ggcgtggaat gagacaaacg	2259
30	cggccataac agcggaaatga caccggtaaa ccgaaaggca ggaacaggag agcgcacgag	2319
	ggagccgcca ggggaaacgc ctggatatctt tatagtctctg tcgggtttcg ccaccactga	2379
35	tttgagcgtc agatttcgtg atgcttgtca gggggggcga gcctatggaa aaacggcttt	2439
	gcgcgggcc tctcacttcc ctgttaagta tcttcctggc atcttccagg aaatctccgc	2499
	cccggttcgta agccatttcc gctcgcgcga gtgcgaacgac cgagcgtagc gagtcagtga	2559
40	gcgaggaagc ggaatatatc ctgtatcaca tattctgctg acgcaccggg gcagcctttt	2619
	ttctcctgcc acatgaagca cttcactgac accctcatca gtgccaacat agtaagccag	2679
45	tatacactcc gctagcgtg atgtccggcg gtgcttttgc cgttacgcac caccctgtca	2739
	gtagctgaac aggagggaca gctgatagaa acagaagcca ctggagcacc tcaaaaacac	2799
	catcatacac taaatcagta agttggcagc atcaccgcac gcaactttgcg ccgaataaat	2859
50	acctgtgacg gaagatcact tcgcagaata aataaatcct ggtgtccctg ttgataccgg	2919
	gaagccctgg gccaaactttt ggcgaaaatg agacgttgat cggcacgtaa gaggttccaa	2979
55	ctttcaccat aatgaaataa gatcactacc gggcgtattt tttgagttat cgagattttc	3039
	aggagctaag gaagctaaaa tggagaaaaa aatcactgga tataccaccg ttgatataac	3099
	ccaatggcat cgtaaagaac attttgaggc atttcagtca gttgctcaat gtacctataa	3159

	ccagaccgtt	cagctggata	ttacggcctt	tttaaagacc	gtaaagaaaa	ataagcacia	3219
	gttttatccg	gcctttattc	acattcttgc	ccgcctgatg	aatgctcatc	cggaattccg	3279
5	tatggcaatg	aaagacggtg	agctggatg	atgggatagt	gttcaccctt	gttacaccgt	3339
	tttccatgag	caaactgaaa	cgttttcatc	gctctggagt	gaataccacg	acgatttccg	3399
10	gcagtttcta	cacatatatt	cgcaagatgt	ggcgtgttac	ggtgaaaacc	tggcctattt	3459
	ccctaaaggg	tttattgaga	atatgttttt	cgtctcagcc	aatccctggg	tgagtttcac	3519
	cagttttgat	ttaaacgtgg	ccaatatgga	caacttcttc	gcccccgttt	tcaccatggg	3579
15	caaataattat	acgcaaggcg	acaagggtgct	gatgccgctg	gcgattcagg	ttcatcatgc	3639
	cgtctgtgat	ggcttccatg	tcggcagaat	gcttaatgaa	ttacaacagt	actgcgatga	3699
20	gtggcagggc	ggggcgtaat	ttttttaagg	cagttattgg	tgcccttaaa	cgcctgggtgc	3759
	tacgcctgaa	taagtataaa	taagcggatg	aatggcagaa	attcgaaagc	aaattcgacc	3819
	cggtcgtcgg	ttcagggcag	ggtcgtaaaa	tagccgctta	tgtctattgc	tggtttaccg	3879
25	gtttattgac	taccggaagc	agtgtgaccg	tgtgcttctc	aaatgcctga	ggccagtttg	3939
	ctcaggctct	ccccgtggag	gtaataattg	acgatatgat	catttattct	gcctcccaga	3999
30	gcctgataaa	aacgggttagc	gcttcgttaa	tacagatgta	ggtgttccac	agggtagcca	4059
	gcagcatcct	gcgatgcaga	tccggaacat	aatggtgcag	ggcgcttggt	tcggcggtggg	4119
	tatggtggca	ggccccgtgg	ccgggggact	gttgggcgct	gccggcacct	gtcctacgag	4179
35	ttgcatgata	aagaagacag	tcataagtgc	ggcgacgata	gtcatgcccc	gcgcccaccg	4239
	gaaggagcta	ccggacagcg	gtgcggactg	ttgtaactca	gaataagaaa	tgaggccgct	4299
40	catggcgttg	actctcagtc	atagtatcgt	ggtatcaccg	gttggttcca	ctctctgttg	4359
	cgggcaactt	cagcagcacg	taggggactt	ccgcgtttcc	agactttacg	aaacacggaa	4419
	accgaagacc	attcatgttg	ttgctcaggt	cgcagacgtt	ttgcagcagc	agtcgcttca	4479
45	cgttcgctcg	cgtatcggtg	attcattctg	ctaaccagta	aggcaacccc	gccagcctag	4539
	ccgggtcctc	aacgacagga	gcacgatcat	gcgcacccgt	ggccaggacc	caacgctgcc	4599
50	cgagatgogc	cgcgtgcggc	tgctggagat	ggcggacgcg	atggatatgt	tctgccaaagg	4659
	gttggtttgc	gcattcacag	ttctccgcaa	gaattgattg	gtccaattc	ttggagtggg	4719
	gaatccgtta	gcgaggtgcc	gccggcttcc	attcaggtcg	aggtggcccc	gctccatgca	4779
55	ccgcgacgca	acgcggggag	gcagacaagg	tatagggcgg	cgcctacaat	ccatgccaac	4839
	ccgttccatg	tgctcgccga	ggcggcataa	atcgccgtga	cgatcagcgg	tccagtgatc	4899
	gaagttaggc	tggttaagagc	cgcgagcgat	ccttgaagct	gtccctgatg	gtcgtcatct	4959

acctgcctgg acagcatggc ctgcaacgcg ggcattcccga tgccgccgga agcgagaaga 5019  
 5 atcataatgg ggaaggccat ccagcctcgc gtcgcgaacg ccagcaagac gtagcccagc 5079  
 gcgtcggccg ccatgccggc gataatggcc tgcttctcgc cgaaacgttt ggtggcgggga 5139  
 ccagtgcga aggcttgagc gaggcggtgc aagattccga ataccgcaag cgacaggccg 5199  
 10 atcatcgtcg cgctccagcg aaagcggtcc tcgccgaaaa tgaccagag cgctgccggc 5259  
 acctgtccta cgagttgcat gataaagaag acagtcataa gtgcggcgac gatagtcatg 5319  
 ccccgcgccc accggaagga gctgactggg ttgaaggctc tcaagggcat cggtcgacgc 5379  
 15 tctcccttat gcgactcctg cattaggaag cagcccagta gtaggttgag gccgttgagc 5439  
 accgccgccc caaggaatgg tgcattgcac gatcaccaca attcagcaaa ttgtgaacat 5499  
 20 catcacgttc atctttccct ggttgccaat ggcccatttt cctgtcagta acgagaaggt 5559  
 cgcgcaattca ggcgcttttt agactggctg taatgaac 5597

25 <210> 12  
 <211> 574  
 <212> PRT  
 <213> Unknown

30 <220>  
 <223> Plasmid  
 <400> 12

35 Met Asp Ile Gln Lys Arg Val Ser Asp Met Glu Pro Lys Thr Lys Lys  
 1 5 10 15

40 Gln Arg Ser Leu Tyr Ile Pro Tyr Ala Gly Pro Val Leu Leu Glu Phe  
 20 25 30

45 Pro Leu Leu Asn Lys Gly Ser Ala Phe Ser Met Glu Glu Arg Arg Asn  
 35 40 45

Phe Asn Leu Leu Gly Leu Leu Pro Glu Val Val Glu Thr Ile Glu Glu  
 50 55 60

50 Gln Ala Glu Arg Ala Trp Ile Gln Tyr Gln Gly Phe Lys Thr Glu Ile  
 65 70 75 80

55 Asp Lys His Ile Tyr Leu Arg Asn Ile Gln Asp Thr Asn Glu Thr Leu  
 85 90 95

Phe Tyr Arg Leu Val Asn Asn His Leu Asp Glu Met Met Pro Val Ile

	100	105	110
5	Tyr Thr Pro Thr Val Gly Ala Ala Cys Glu Arg Phe Ser Glu Ile Tyr 115 120 125		
10	Arg Arg Ser Arg Gly Val Phe Ile Ser Tyr Gln Asn Arg His Asn Met 130 135 140		
15	Asp Asp Ile Leu Gln Asn Val Pro Asn His Asn Ile Lys Val Ile Val 145 150 155 160		
20	Val Thr Asp Gly Glu Arg Ile Leu Gly Leu Gly Asp Gln Gly Ile Gly 165 170 175		
25	Gly Met Gly Ile Pro Ile Gly Lys Leu Ser Leu Tyr Thr Ala Cys Gly 180 185 190		
30	Gly Ile Ser Pro Ala Tyr Thr Leu Pro Val Val Leu Asp Val Gly Thr 195 200 205		
35	Asn Asn Gln Gln Leu Leu Asn Asp Pro Leu Tyr Met Gly Trp Arg Asn 210 215 220		
40	Pro Arg Ile Thr Asp Asp Glu Tyr Tyr Glu Phe Val Asp Glu Phe Ile 225 230 235 240		
45	Gln Ala Val Lys Gln Arg Trp Pro Asp Val Leu Leu Gln Phe Glu Asp 245 250 255		
50	Phe Ala Gln Lys Asn Ala Met Pro Leu Leu Asn Arg Tyr Arg Asn Glu 260 265 270		
55	Ile Cys Ser Phe Asn Asp Asp Ile Gln Gly Thr Ala Ala Val Thr Val 275 280 285		
60	Gly Thr Leu Ile Ala Ala Ser Arg Ala Ala Gly Gly Gln Leu Ser Glu 290 295 300		
65	Lys Lys Ile Val Phe Leu Gly Ala Gly Ser Ala Gly Cys Gly Ile Ala 305 310 315 320		
70	Glu Met Ile Ile Ser Gln Thr Gln Arg Glu Gly Leu Ser Glu Glu Ala 325 330 335		

Ala Arg Gln Lys Val Phe Met Val Asp Arg Phe Gly Leu Leu Thr Asp  
340 345 350

5 Lys Met Pro Asn Leu Leu Pro Phe Gln Thr Lys Leu Val Gln Lys Arg  
355 360 365

10 Glu Asn Leu Ser Asp Trp Asp Thr Asp Ser Asp Val Leu Ser Leu Leu  
370 375 380

15 Asp Val Val Arg Asn Val Lys Pro Asp Ile Leu Ile Gly Val Ser Gly  
385 390 395 400

Gln Thr Gly Leu Phe Thr Glu Glu Ile Ile Arg Glu Met His Lys His  
405 410 415

20 Cys Pro Arg Pro Ile Val Met Pro Leu Ser Asn Pro Thr Ser Arg Val  
420 425 430

25 Glu Ala Thr Pro Gln Asp Ile Ile Ala Trp Thr Glu Gly Asn Ala Leu  
435 440 445

30 Val Ala Thr Gly Ser Pro Phe Asn Pro Val Val Trp Lys Asp Lys Ile  
450 455 460

35 Tyr Pro Ile Ala Gln Cys Asn Asn Ala Phe Ile Phe Pro Gly Ile Gly  
465 470 475 480

Leu Gly Val Ile Ala Ser Gly Ala Ser Arg Ile Thr Asp Glu Met Leu  
485 490 495

40 Met Ser Ala Ser Glu Thr Leu Ala Gln Tyr Ser Pro Leu Val Leu Asn  
500 505 510

45 Gly Glu Gly Met Val Leu Pro Glu Leu Lys Asp Ile Gln Lys Val Ser  
515 520 525

50 Arg Ala Ile Ala Phe Ala Val Gly Lys Met Ala Gln Gln Gln Gly Val  
530 535 540

55 Ala Val Lys Thr Ser Ala Glu Ala Leu Gln Gln Ala Ile Asp Asp Asn  
545 550 555 560

Phe Trp Gln Ala Glu Tyr Arg Asp Tyr Arg Arg Thr Ser Ile  
565 570

<210> 13  
 <211> 5068  
 <212> DNA  
 5 <213> Artificial  
  
 <220>  
 <223> Plasmid  
  
 10 <400> 13  
 tatgtatccg gatttaaaag gaaaagtcgt cgctattaca ggagctgctt cagggctcgg 60  
 aaaggcgatg gccattcgct tcggcaagga gcaggcaaaa gtggttatca actattatag 120  
 15 taataaacia gatccgaacg aggtaaaaga agaggctcatc aaggcgggag gtgaagctgt 180  
 tgtcgtccaa ggagatgtca cgaaagagga agatgtaaaa aatatcgtgc aaacggcaat 240  
 taaggagtgc gccacactcg atattatgat taataatgcc ggtcttgaaa atcctgtgcc 300  
 20 atctcacgaa atgccgctca aggattggga taaagtcatc gccacgaact taacgggtgc 360  
 ctttttagga agccgtgaag cgattaaata tttcgtagaa aacgatatca agggaaatgt 420  
 25 cattaacatg tccagtgtgc acgaagtgat tccttggccg ttatttgtcc actatgcggc 480  
 aagtaaaggc gggataaagc tgatgacaga aacattagcg ttggaatacg cgccgaaggg 540  
 cattcgcgtc aataatattg ggccaggtgc gatcaacacg ccaatcaatg ctgaaaaatt 600  
 30 cgctgaccct aaacagaaag ctgatgtaga aagcatgatt ccaatgggat atatcggcga 660  
 accggaggag atcgccgcag tagcagcctg gcttgcttcg aaggaagcca gctacgtcac 720  
 35 aggcacacg ttattcgcgg acggcgggtat gacacaatat ccttcattcc aggcaggccg 780  
 cggttaatag tagaagcttc tgttttggcg gatgagagaa gattttcagc ctgatacaga 840  
 ttaaatacaga acgcagaagc ggtctgataa aacagaattt gcctggcgcc agtagcgcg 900  
 40 tgggtcccacc tgaccccatg ccgaactcag aagtgaacg ccgtagcgcc gatggtagtg 960  
 tggggtctcc ccatgcgaga gtaggggaact gccaggcatc aaataaaacg aaaggctcag 1020  
 45 tcgaaagact gggcctttcg ttttatctgt tgtttgtcgg tgaacgctct cctgagtagg 1080  
 acaaataccg cgaggagcga tttgaacgtt gcgaagcaac ggcccgagg gtggcgggca 1140  
 ggacgcccgc cataaactgc caggcatcaa attaagcaga aggcacatcct gacggatggc 1200  
 50 ctttttgcgt ttctacaaac tcttttgttt atttttctaa atacattcaa atatgtatcc 1260  
 gctcatgaga caataaccct gataaatgct tcaataatat tgaaaaagga agagtatgag 1320  
 55 tattcaacat ttccgtgtcg cccttattcc ctttttgcg gcattttgcc ttctgtttt 1380  
 tgctcaccga gaaacgctgg tgaaagtaaa agatgctgaa gatcagttgg gtgcacgagt 1440  
 gggttacatc gaactggatc tcaacagcgg taagatcctt gagagttttc gcccgaaga 1500

	acgtttttcca atgatgagca ctttttaaagt tctgctatgt ggcgcggtat tatcccgtgt	1560
5	tgacgcccgg caagagcaac tcggtcgccc catacactat tctcagaatg acttggttga	1620
	gtactcacca gtcacagaaa agcatcttac ggatggcatg acagtaagag aattatgcag	1680
	tgctgccata accatgagtg ataacactgc ggccaactta cttctgacaa cgatcggagg	1740
10	accgaaggag ctaaccgctt ttttgcacaa catgggggat catgtaactc gccttgatcg	1800
	ttgggaaccg gagctgaatg aagccatacc aaacgacgag cgtgacacca cgatgcctgt	1860
15	agcaatggca acaacgttgc gcaaactatt aactggcgaa ctacttactc tagcttcccg	1920
	gcaacaatta atagactgga tggaggcgga taaagttgca ggaccacttc tgcgctcggc	1980
	ccttcgggct ggctggttta ttgctgataa atctggagcc ggtgagcgtg ggtctcgcgg	2040
20	tatcattgca gcaactatgg atgaacgaaa tagacagatc gctgagatag gtgcctcact	2100
	ggggagtcag gcaactatgg atgaacgaaa tagacagatc gctgagatag gtgcctcact	2160
	gattaagcat tggttaactgt cagaccaagt ttactcatat atactttaga ttgatttaaa	2220
25	acttcatttt taatttaaaa ggatctaggt gaagatcctt tttgataatc tcatgaccaa	2280
	aatcccttaa cgtgagtttt cgttccactg agcgtcagac cccgtagaaa agatcaaagg	2340
30	atcttcttga gatccttttt ttctgcgcgt aatctgctgc ttgcaaacaa aaaaaccacc	2400
	gctaccagcg gtggtttgtt tgccggatca agagctacca actctttttc cgaaggtaac	2460
35	tggtttcagc agagcgcaga taccaaatac tgtccttcta gtgtagccgt agttaggcca	2520
	ccacttcaag aactctgtag caccgcctac atacctcgct ctgctaatac tgttaccagt	2580
	ggctgctgcc agtggcgata agtcgtgtct taccgggttg gactcaagac gatagttacc	2640
40	ggataaggcg cagcggtcgg gctgaacggg gggttcgtgc acacagccca gcttggagcg	2700
	aacgacctac accgaactga gatacctaca gcgtgagcta tgagaaagcg ccacgcttcc	2760
45	cgaagggaga aaggcggaca ggtatccggt aagcggcagg gtcggaacag gagagcgac	2820
	gagggagctt ccagggggaa acgcctggta tctttatagt cctgtcgggt ttccgccact	2880
	ctgacttgag cgtcgatttt tgtgatgctc gtcagggggg cggagcctat ggaaaaacgc	2940
50	cagcaacgcg gcctttttac ggttcctggc cttttgctgg ccttttgctc acatgttctt	3000
	tcctgcgtta tcccctgatt ctgtggataa ccgtattacc gcctttgagt gagctgatac	3060
55	cgctcgccgc agccgaacga ccgagcgcag cgagtcagtg agcgaggaag cggaagagcg	3120
	cctgatgcgg tattttctcc ttacgcactc gtgcggtatt tcacaccgca tatatggtgc	3180
	actctcagta caatctgctc tgatgccgca tagttaagcc agtatacact ccgctatcgc	3240



	tacgtgactg	ggatcatggct	gcgccccgac	acccgccaac	acccgctgac	gcgcccctgac	3300
	gggcttgtct	gctcccggca	tccgcttaca	gacaagctgt	gaccgtctcc	gggagctgca	3360
5	tgtgtcagag	gttttcaccg	tcatcaccga	aacgcgcgag	gcagctgcgg	taaagctcat	3420
	cagcgtggtc	gtgaagcgat	tcacagatgt	ctgcctgttc	atccgcgtcc	agctcgttga	3480
	gtttctccag	aagcgttaat	gtctggcttc	tgataaagcg	ggccatgtta	agggcggttt	3540
10	tttcctgttt	ggtcacttga	tgccctccgtg	taagggggaa	tttctgttca	tgggggtaat	3600
	gataccgatg	aaacgagaga	ggatgctcac	gatacgggtt	actgatgatg	aacatgcccc	3660
15	gttactggaa	cggtgtgagg	gtaaacaact	ggcggatagg	atgcggcggg	accagagaaa	3720
	aatcactcag	ggatcaatgcc	agcgtctcgt	taatacagat	gtagggtgttc	cacagggtag	3780
	ccagcagcat	cctgcgatgc	agatccggaa	cataatgggtg	cagggcgctg	acttccgcgt	3840
20	ttccagactt	tacgaaacac	ggaaaccgaa	gaccattcat	gttggtgtct	aggtcgcaga	3900
	cgttttgcag	cagcagtcgc	ttcacgttcg	ctcgcgtatc	ggtgattcat	tctgctaacc	3960
25	agtaaggcaa	ccccgccagc	ctagccgggt	cctcaacgac	aggagcacga	tcatgcgcac	4020
	ccgtggccag	gacccaacgc	tgcccagagat	gcgccgcgtg	cggctgctgg	agatggcgga	4080
	cgcgatggat	atgtttctgcc	aaggggttgg	ttgcgcattc	acagttctcc	gcaagaattg	4140
30	attggctcca	attcttggag	tggatgaatcc	gttagcgagg	tgccgccggc	ttccattcag	4200
	gtcgaggtgg	cccggctcca	tgcaccgcga	cgcaacgcgg	ggaggcagac	aaggatatagg	4260
35	gcggcggcgc	ctacaatcca	tgccaacccg	ttccatgtgc	tcgccgaggg	ggcataaata	4320
	gccgtgacga	tcagcgggtcc	agtgatcgaa	gttaggctgg	taagagccgc	gagcgatcct	4380
	tgaagctgtc	cctgatgggtc	gtcatctacc	tgccctggaca	gcatggcctg	caacgcgggc	4440
40	atcccgatgc	cgccggaagc	gagaagaatc	ataatgggga	aggccatcca	gcctcgcgtc	4500
	gcgaacgcca	gcaagacgta	gcccagcgcg	tcggccgccca	tgccggcgat	aatggcctgc	4560
45	ttctcgcgca	aacgttttgg	ggcgggacca	gtgacgaagg	cttgagcgag	ggcgtgcaag	4620
	attccgaata	ccgcaagcga	caggccgatc	atcgtcgcgc	tccagcgaaa	gcggtcctcg	4680
	ccgaaaatga	cccagagcgc	tgccggcacc	tgctctacga	gttgcatgat	aaagaagaca	4740
50	gtcataagtg	cggcgacgat	agtcatgccc	cgcgcccacc	ggaaggagct	gactgggttg	4800
	aaggctctca	agggcatcgg	tcgacgtctc	cccttatgcg	actcctgcat	taggaagcag	4860
55	cccagtagta	ggttgaggcc	gttgagcacc	gccgcgcgca	ggaatgggtg	atgcatcgat	4920
	caccacaatt	cagcaaattg	tgaacatcat	cacgttcatc	tttccttggg	tgccaatggc	4980
	ccattttcct	gtcagtaacg	agaaggtcgc	gaattcaggc	gctttttaga	ctggtcgtaa	5040

tgaacaattc ttaagaagga gatataca

5068